

On page 23, please replace the paragraph starting on line 31 with the following:

AB
Figure 2 shows the predicted amino acid sequence (SEQ ID NO:2) of an exemplary BGL4 polypeptide based on the nucleotide sequence provided in Figure 1 (SEQ ID NO:1). The predicted molecular weight of the encoded BGL4 polypeptide is 90.7kDa. No sequence resembling a signal peptide (Nielsen, H., Engelbrecht, J., Brunak, S., von Heijne, G., Protein Engineering, 10:1-6, 1997) is present at the amino terminus of BGL4 suggesting that the BGL4 polypeptide is not secreted.

On page 24, please replace the paragraph starting on line 1 with the following:

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AJT
A Basic BLASTP search (www.ncbi.nlm.nih.gov/BLAST) of the non-redundant protein database, conducted on September 11, 2001 with the BGL4 amino acid sequence indicated 46% sequence identity to GenBank Accession Number X05918 (beta-glucosidase precursor of *Kluyveromyces marxianus*), 45% sequence identity to GenBank Accession Number AL355920 (beta-glucosidase precursor of *Schizosaccharomyces pombe*), 42% sequence identity to GenBank Accession Number AF329731 (beta-glucosidase of *Volvariella volvacea*), and 41% sequence identity to GenBank Accession Number AJ293760 (putative beta-glucosidase of *Agaricus bisporus*). The ten sequences having highest identity but less than 46% identity with BGL4 were all annotated as beta-glucosidases. These sequence similarities indicate that BGL4 is a member of glycosyl hydrolase family 3 (Henrissat, B. and Bairoch, A. (1993) Biochem. J. 293:781-788).

On page 28, please replace the paragraph starting on line 26 with the following:

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Preferred culture conditions for a given filamentous fungus may be found in the scientific literature and/or from the source of the fungi such as the American Type Culture Collection (ATCC; www.atcc.org/). After fungal growth has been established, the cells are exposed to conditions effective to cause or permit the over expression of BGL4.

On page 37, please replace the paragraph starting on line 19 with the following:

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Exemplary computer programs which can be used to determine identity between two sequences include, but are not limited to, the suite of BLAST programs, e.g., BLASTN, BLASTX, and TBLASTX, BLASTP and TBLASTN, publicly available on the Internet at www.ncbi.nlm.nih.gov/BLAST/. See also, Altschul, et al., 1990 and Altschul, et al., 1997.

On page 40, please replace the paragraph starting on line 9 with the following: